APPENDIX

Amended and Added Claims

21. A method for detecting a genetic abnormality on chromosome 12q15 in a patient, comprising:

obtaining a genetic sample from a patient;

producing a first reaction product by incubating the genetic sample with a polynucleotide comprising at least 14 contiguous nucleotides of SEQ ID NO:1 or the complement of SEQ ID NO:1, under conditions wherein said polynucleotide will hybridize to complementary polynucleotide sequence;

visualizing the first reaction product; and

comparing said first reaction product to a control reaction product from a wild type patient, wherein a difference between said first reaction product and said control reaction product is indicative of a genetic abnormality on chromosome 12q15 in the patient.

28. A method for detecting inflammation in a patient, comprising:

obtaining a tissue or biological sample from a patient;

labeling a polynucleotide comprising at least 14 contiguous nucleotides of SEQ ID NO:1 or the complement of SEQ ID NO:1;

incubating the tissue or biological sample with under conditions wherein the polynucleotide will hybridize to complementary polynucleotide sequence;

visualizing the labeled polynucleotide in the tissue or biological sample; and

comparing the level of labeled polynucleotide hybridization in the tissue or biological sample from the patient to a normal control tissue or biological sample,

wherein an increase in the labeled polynucleotide hybridization to the patient tissue or biological sample relative to the normal control tissue or biological sample is indicative of inflammation in the patient.

29. A method for detecting activated T-cells in a patient, comprising:

obtaining a tissue or biological sample from a patient;

labeling a polynucleotide comprising at least 14 contiguous nucleotides of SEQ ID NO:1 or the complement of SEQ ID NO:1;

incubating the tissue or biological sample with under conditions wherein the polynucleotide will hybridize to complementary polynucleotide sequence;

visualizing the labeled polynucleotide in the tissue or biological sample; and

comparing the level of labeled polynucleotide hybridization in the tissue or biological sample from the patient to a normal control tissue or biological sample,

wherein an increase in the labeled polynucleotide hybridization to the patient tissue or biological sample relative to the normal control tissue or biological sample is indicative of activated T-cells in the patient.

30. The method according to claim 29, wherein the activated T-cells are CD3+ T-cells.

31. The method according to claim 28, wherein the inflammation is cause from an inflammatory disease comprising arthritis, asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, pancreatitis, sepsis, and endotoxemia.

32. The method according to claim 21, wherein the genetic abnormality further comprises a gross chromosomal abnormality, a translocation, aneuploidy, large insertion, large deletion, chromosome rearrangement, or a chromosome break.